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## OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:30 ; Search time 66.75 Seconds

(without alignments)  
37.620 Million cell updates/sec

Title: US-09-846-033B-36

Perfect score: 1 DRSNLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 7

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp190s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	7	4	AAB84241	AAB84241 Zinc prot
2	100.0	7	5	ABB80798	ABD80798 Human ER-
3	100.0	7	5	ABB80812	ABD80812 Human ER-
4	100.0	7	5	ABP50162	ABP50162 Zinc fmg
5	100.0	7	5	ABP50914	ABP50914 Zinc fmg
6	100.0	7	5	ABP51092	ABP51092 Zinc fmg
7	100.0	7	5	ABP50535	ABP50535 Zinc fmg
8	100.0	7	5	ABP49313	ABP49313 Zinc fmg
9	100.0	7	5	ABP50277	ABP50277 Zinc fmg
10	100.0	7	5	ABP50373	ABP50373 Zinc fmg
11	100.0	7	5	ABP48386	ABP48386 Zinc fmg
12	100.0	7	5	ABP49231	ABP49231 Zinc fmg
13	100.0	7	5	ABP49241	ABP49241 Zinc fmg
14	100.0	7	5	ABP49259	ABP49259 Zinc fmg
15	100.0	7	5	ABP49880	ABP49880 Zinc fmg
16	100.0	7	5	ABP50861	ABP50861 Zinc fmg
17	100.0	7	5	ABP50538	ABP50538 Zinc fmg
18	100.0	7	5	ABP50920	ABP50920 Zinc fmg
19	100.0	7	5	ABP50858	ABP50858 Zinc fmg
20	100.0	7	5	ABP49274	ABP49274 Zinc fmg
21	100.0	7	5	ABP50311	ABP50311 Zinc fmg
22	100.0	7	5	ABP51150	ABP51150 Zinc fmg
23	100.0	7	5	ABP49769	ABP49769 Zinc fmg
24	100.0	7	5	ABP51159	ABP51159 Zinc fmg
25	100.0	7	5	ABP51180	ABP51180 Zinc fmg

26	7	100.0	7	5	ABP49201	ABP49201 Zinc fmg
27	7	100.0	7	5	ABP49224	ABP49224 Zinc fmg
28	7	100.0	7	5	ABP49666	ABP49666 Zinc fmg
29	7	100.0	7	5	ABP49958	ABP49958 Zinc fmg
30	7	100.0	7	5	ABP50823	ABP50823 Zinc fmg
31	7	100.0	7	5	ABP51101	ABP51101 Zinc fmg
32	7	100.0	7	5	ABP51147	ABP51147 Zinc fmg
33	7	100.0	7	5	ABP49964	ABP49964 Zinc fmg
34	7	100.0	7	5	ABP50254	ABP50254 Zinc fmg
35	7	100.0	7	5	ABP50521	ABP50521 Zinc fmg
36	7	100.0	7	5	ABP50524	ABP50524 Zinc fmg
37	7	100.0	7	5	ABP50542	ABP50542 Zinc fmg
38	7	100.0	7	5	ABP50545	ABP50545 Zinc fmg
39	7	100.0	7	5	ABP50166	ABP50166 Zinc fmg
40	7	100.0	7	5	ABP49157	ABP49157 Zinc fmg
41	7	100.0	7	5	ABP50056	ABP50056 Zinc fmg
42	7	100.0	7	5	ABJ03824	ABJ03824 Human VEG
43	7	100.0	7	5	ABJ03812	ABJ03812 Human VEG
44	7	100.0	7	5	ABJ03888	ABJ03888 Human VEG
45	7	100.0	7	5	ABJ03910	ABJ03910 Human VEG

## ALIGNMENTS

RESULT 1  
AAB84241 standard; peptide, 7 AA.  
ID AAB84241

AC AAB84241;

DT 06-AUG-2001 (first entry)

DE Zinc protein recognition helix SB89 for target DNA triplet GAC.

KW Phenotype associated gene; zinc finger protein; cancer; nephritis;  
KW prostate hypertrophy; hematoptosis; osteoporosis; obesity;

KM cardiovascular disease; diabetes.

OS Synthetic.

PN WO200140798-A2.

PD 07-JUN-2001.

PF 06-DEC-2000; 2000WO-US033086.

PR 06-DEC-1999; 99US-00456100.

(SANG-) SANGAMO BIOSCIENCES INC.

Case CC, Liu Q, Rabar EJ;

WPI; 2001-374953/39.

Identifying genes associated with selected phenotype for research purposes, involves culturing cells transduced with nucleic acid encoding zinc finger proteins and assaying cells exhibiting selected phenotype.

Example 1; Page 36; 58pp; English.

The specification describes a method for identifying genes associated with a selected phenotype. The method involves providing a library of nucleotide sequences encoding partially randomized zinc finger proteins, transducing cells with expression vectors, each comprising a sequence from the library, culturing the cells for expressing the zinc finger protein, assaying the cells for selected phenotype, and identifying the gene of interest, in cells exhibiting the phenotype. The method is useful for identifying a gene or genes associated with a selected phenotype such as the one related to cancer, nephritis, prostate hypertrophy, hematoptosis, osteoporosis, obesity, cardiovascular disease or diabetes. The method is useful in academic laboratories, in the biotechnological industries, and in pharmaceutical, genomic, agricultural and chemical

CC companies. AAB84233-44 represent recognition helices of zinc finger  
CC proteins, which recognise different DNA triplets  
CC  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRSNLTTR 7  
Db 1 DRSNLTTR 7  
RESULT 2  
AAB80798  
ID ABB80798 standard; peptide; 7 AA.  
AC ABB80798;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE Human ER-alpha locus targeting ZFP1 peptide #8.  
XX  
KW ZFP; cytostatic; antidiabetic; ophthalmological; vasotropic; chromatin;  
KW gene expression; antirheumatic; antiarthritic; antiporiatic; nocrotropic;  
KW neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha;  
KW zinc finger protein.  
XX  
OS Synthetic.  
XX  
PN WO200244386-A2.  
XX  
PD 06-JUN-2002.  
XX  
PF 30-NOV-2001; 2001WO-US045098.  
XX  
PR 01-DEC-2000; 2000US-0250804P.  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
PI Wolffe AP, Tse C, Collingwood T;  
XX  
DR WPI; 2002-537455/57.  
XX  
PT Regulating expression of gene by contacting cell with regulatory molecule  
PT comprising DNA-binding domain targeted to sequence within accessible  
PT region of cellular chromatin associated with a gene, and functional  
PT domain.  
XX  
PS Example 1; Page 44; 64pp; English.  
XX  
CC The invention relates to regulating the expression of a gene residing in  
CC the chromatin of a cell. The method involves identifying one or more  
CC accessible regions in cellular chromatin associated with gene; designing  
CC a regulatory molecule, where the regulatory molecule comprises a DNA-  
CC binding domain targeted to a sequence within the accessible region, and a  
CC functional domain; and contacting the regulatory molecule with the cell.  
CC The method is used for regulating the expression of a gene (e.g., a gene  
CC encoding a nuclear receptor such as estrogen receptor alpha (ERalpha),  
CC estrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha  
CC (HNF4alpha), hepatocyte nuclear factor 4 gamma (HNF4gamma), peroxisome  
CC proliferator activated receptor gamma (PPARGgamma), retinoid X receptor  
CC alpha (RXRalpha), or constitutively active receptor alpha (CARalpha))  
CC residing in the chromatin of a cell. Regulation of gene expression (such  
CC as nuclear receptor genes) will be useful in treatment of various  
CC diseases, including cancer, diabetes and cardiovascular disease, where  
CC the regulatory molecule as described above, is contacted with the cell to  
CC carry out the regulation. The method is also useful for modulation of  
CC gene expression for therapeutic or prophylactic applications e.g.,  
CC diabetic retinopathy, ischemia, macular degeneration, rheumatoid  
CC arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's  
CC disease, stroke, etc. The method also has applications in pharmaceutical

CC research of both nuclear receptors of known function as well as those of  
CC unknown function. The method also facilitates development of tissue and  
CC animal models of disease states; drug validation, and therapeutic product  
CC development. The methods also allow identification of the role of nuclear  
CC receptors of unknown functions in cellular homeostasis. Sequences  
CC ABB80791-817 represent zinc finger protein (ZFP) DNA-binding domains that  
CC were fused to functional domains and tested for their ability to regulate  
CC expression of the ER in living cells  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRSNLTTR 7  
Db 1 DRSNLTTR 7  
RESULT 3  
AAB80812  
ID ABB80812 standard; peptide; 7 AA.  
AC ABB80812;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE Human ER-alpha locus targeting ZFP3 peptide #4.  
XX  
DE  
XX  
KW ZFP; cytostatic; antidiabetic; ophthalmological; vasotropic; chromatin;  
KW gene expression; antirheumatic; antiarthritic; antiporiatic; nocrotropic;  
KW neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha;  
KW zinc finger protein.  
XX  
OS Synthetic.  
XX  
PN WO200244386-A2.  
XX  
PD 06-JUN-2002.  
XX  
PF 30-NOV-2001; 2001WO-US045098.  
XX  
PR 01-DEC-2000; 2000US-0250804P.  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
PI Wolffe AP, Tse C, Collingwood T;  
XX  
DR WPI; 2002-537455/57.  
XX  
PT Regulating expression of gene by contacting cell with regulatory molecule  
PT comprising DNA-binding domain targeted to sequence within accessible  
PT region of cellular chromatin associated with a gene, and functional  
PT domain.  
XX  
PS Example 1; Page 44; 64pp; English.  
XX  
CC The invention relates to regulating the expression of a gene residing in  
CC the chromatin of a cell. The method involves identifying one or more  
CC accessible regions in cellular chromatin associated with gene; designing  
CC a regulatory molecule, where the regulatory molecule comprises a DNA-  
CC binding domain targeted to a sequence within the accessible region, and a  
CC functional domain; and contacting the regulatory molecule with the cell.  
CC The method is used for regulating the expression of a gene (e.g., a gene  
CC encoding a nuclear receptor such as estrogen receptor alpha (ERalpha),  
CC estrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha  
CC (HNF4alpha), hepatocyte nuclear factor 4 gamma (HNF4gamma), peroxisome  
CC proliferator activated receptor gamma (PPARGgamma), retinoid X receptor  
CC alpha (RXRalpha), or constitutively active receptor alpha (CARalpha))  
CC residing in the chromatin of a cell. Regulation of gene expression (such  
CC as nuclear receptor genes) will be useful in treatment of various  
CC diseases, including cancer, diabetes and cardiovascular disease, where

CC the regulatory molecule as described above, is contacted with the cell to  
CC carry out the regulation. The method is also useful for modulation of  
CC gene expression for therapeutic or prophylactic applications e.g.,  
CC diabetic retinopathy, ischaemia, macular degeneration, rheumatoid  
CC arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's  
CC disease, stroke, etc. The method also has applications in pharmaceutical  
CC research of both nuclear receptors of known function as well as those of  
CC unknown function. The method also facilitates development of tissue and  
CC animal models of disease states, drug validation, and therapeutic product  
CC development. The methods also allow identification of the role of nuclear  
CC receptors of unknown functions in cellular homeostasis. Sequences  
CC AB880791-817 represent zinc finger protein (ZFP) DNA-binding domains that  
CC were fused to functional domains and tested for their ability to regulate  
CC expression of the ER in living cells  
CC  
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTNR 7  
Db 1 DRSNLTNR 7

RESULT 4  
ABP50162  
ID ABP50162 standard; peptide; 7 AA.

AC ABP50162;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:3666.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

PD 30-MAY-2002.

PF 20-NOV-2001; 2001WO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 57; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target subsequence. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (1) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target subsequence, selecting the F2 zinc finger such that it  
CC binds to the S2 target subsequence, and selecting the F3 zinc finger such  
CC that it binds to the S3 target subsequence, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subsequences  
CC having the nucleotide G in the 5'-most position of the subsequence. (I) is

CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention  
CC  
SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTNR 7  
Db 1 DRSNLTNR 7

RESULT 5  
ABP50914  
ID ABP50914 standard; peptide; 7 AA.

AC ABP50914;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:3417.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

PD 30-MAY-2002.

PF 20-NOV-2001; 2001WO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 62; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target subsequence. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (1) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target subsequence, selecting the F2 zinc finger such that it  
CC binds to the S2 target subsequence, and selecting the F3 zinc finger such  
CC that it binds to the S3 target subsequence, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subsequences  
CC having the nucleotide G in the 5'-most position of the subsequence. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid

CC in a sample, and in assays to determined the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7  
Db 1 DRSNLTR 7

RESULT 6  
ABP51092

ID ABP51092 standard; peptide; 7 AA.

AC ABP51092;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:3976.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

PD 30-MAY-2002.

PF 20-NOV-2001; 2001MO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 63; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determined the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc

CC finger peptides which are given in the exemplification of the present  
CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7  
Db 1 DRSNLTR 7

RESULT 7  
ABP50535

ID ABP50535 standard; peptide; 7 AA.

AC ABP50535;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:2791.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

PD 30-MAY-2002.

PF 20-NOV-2001; 2001MO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 59; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determined the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTTR 7  
Db 1 DRSNLTTR 7

RESULT 8  
ABP49313  
ID ABP49313 standard; peptide; 7 AA.

AC ABP49313;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:1577.

DE Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

PD 30-MAY-2002.

PF 20-NOV-2001; 2001WO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 48; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (I1) comprising (I); (2) a polynucleotide (I11) encoding (I) or (I1); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I1), (I1) or (I11) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject. In  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I1) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

CC Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTTR 7  
Db 1 DRSNLTTR 7

RESULT 9  
ABP50277  
ID ABP50277 standard; peptide; 7 AA.

AC ABP50277;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:2705.

DE Zinc finger protein; ZFP; DNA binding protein; zinc finger.

OS Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

PD 30-MAY-2002.

PF 20-NOV-2001; 2001WO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 57; 81pp; English.

CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (I1) comprising (I); (2) a polynucleotide (I11) encoding (I) or (I1); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I1), (I1) or (I11) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject. In  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I1) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

CC Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTTR 7  
Db 1 DRSNLTTR 7

RESULT 10  
ABP50373  
ID ABP50373 standard; peptide; 7 AA.  
XX  
AC ABP50373;  
XX  
DT 28-AUG-2002 (first entry)  
XX  
DE Zinc finger protein related peptide motif SEQ ID NO:2737.  
XX  
KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO200242459-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 20-NOV-2001; 2001WO-US043438.  
XX  
PR 20-NOV-2000; 2000US-00716637.  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
PI Liu Q;  
XX  
DR WPI; 2002-500284/53.  
XX  
PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX  
PS Example 1; Page 58; 81pp; English.  
XX  
CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention  
XX  
SQ Sequence 7 AA;  
XX  
Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRSNLTR 7  
DB 1 DRSNLTR 7  
XX  
RESULT 11  
ABP48386

ID ABP48386 standard; peptide; 7 AA.  
XX  
AC ABP48386;  
XX  
DT 28-AUG-2002 (first entry)  
XX  
DE Zinc finger protein related peptide motif SEQ ID NO:395.  
XX  
KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO200242459-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 20-NOV-2001; 2001WO-US043438.  
XX  
PR 20-NOV-2000; 2000US-00716637.  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
PI Liu Q;  
XX  
DR WPI; 2002-500284/53.  
XX  
PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX  
PS Example 1; Page 37; 81pp; English.  
XX  
CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention  
XX  
SQ Sequence 7 AA;  
XX  
Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRSNLTR 7  
DB 1 DRSNLTR 7  
XX  
RESULT 12  
ABP49231  
ID ABP49231 standard; peptide; 7 AA.  
XX  
AC ABP49231;  
XX

DT 28-AUG-2002 (first entry)  
XX Zinc finger protein related peptide motif SEQ ID NO:1464.  
DE Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
XX  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX MO200242459-A2.  
XX  
XX  
XX 30-MAY-2002.  
XX  
XX 20-NOV-2001; 2001WO-US043438.  
XX  
XX 20-NOV-2000; 2000US-00716637.  
XX  
XX (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
XX Liu Q;  
PI  
XX WPI; 2002-500284/53.  
XX  
XX  
XX New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX  
XX Example 1; Page 48; 81pp; English.  
XX  
XX The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention  
XX  
XX Sequence 7 AA;  
SQ  
Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTTR 7  
| | | | |  
Db 1 DRSNLTTR 7

RESULT 13  
ABP49241  
ID ABP49241 standard; peptide; 7 AA.  
XX  
XX ABP49241;  
AC  
XX 28-AUG-2002 (first entry)  
DT  
XX Zinc finger protein related peptide motif SEQ ID NO:1553.  
DE  
XX  
XX

KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX MO200242459-A2.  
XX  
XX  
XX 30-MAY-2002.  
XX  
XX 20-NOV-2001; 2001WO-US043438.  
XX  
XX 20-NOV-2000; 2000US-00716637.  
XX  
XX (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
XX Liu Q;  
PI  
XX WPI; 2002-500284/53.  
XX  
XX  
XX New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX  
XX Example 1; Page 48; 81pp; English.  
XX  
XX The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention  
XX  
XX Sequence 7 AA;  
SQ  
Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTTR 7  
| | | | |  
Db 1 DRSNLTTR 7

RESULT 14  
ABP49259  
ID ABP49259 standard; peptide; 7 AA.  
XX  
XX ABP49259;  
AC  
XX 28-AUG-2002 (first entry)  
DT  
XX Zinc finger protein related peptide motif SEQ ID NO:1559.  
DE  
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
XX  
XX Homo sapiens.  
OS Synthetic.

```
XX MO200242459-A2.
PN
XX
XX 30-MAY-2002.
PD
XX
XX 20-NOV-2001; 2001WO-US043438.
XX
XX 20-NOV-2000; 2000US-00716637.
XX
XX 20-NOV-2000; 2000US-00716637.
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX Liu Q;
XX
XX WPI; 2002-500284/53.
XX
XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 48; 81bp; English.
XX
XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (i) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. AB071213 to
CC AB072214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
CC
XX
XX Sequence 7 AA;
SQ
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRSNLTNR 7
Db 1 DRSNLTNR 7
RESULT 15
ABP49880
ID ABP49880 standard; peptide: 7 AA.
XX
XX ABP49880;
AC
XX
XX 28-AUG-2002 (first entry)
DT
XX
XX Zinc finger protein related peptide motif SEQ ID NO:3572.
DE
XX
XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
XX MO200242459-A2.
XX
XX 30-MAY-2002.
PD
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XX
XX 20-NOV-2001; 2001WO-US043438.
XX
XX 20-NOV-2000; 2000US-00716637.
XX
XX (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX Liu Q;
XX
XX WPI; 2002-500284/53.
XX
XX New zinc finger protein that binds to target site, useful in studying
PT gene function and for human therapeutics and plant engineering, comprises
PT first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX Example 1; Page 55; 81bp; English.
XX
XX The present invention describes a zinc finger protein (I) that binds to a
CC target site, comprising a first (F1), a second (F2), and a third (F3)
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC and a third (S3) target sub-site. Also described are: (i) a polypeptide
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC that it binds to the S3 target sub-site, thus designing (I) that binds to
CC a target site. (I) is useful for recognition of triplet target sub-sites
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC useful in studying gene function, and for human therapeutics and plant
CC engineering. (I), (II) or (III) is useful in therapeutic methods to
CC modulate the expression of a target region within a subject, in
CC diagnostic methods for sequence specific detection of target nucleic acid
CC in a sample, and in assays to determine the phenotype and function of
CC gene expression. (I) has improved affinity and specificity for their
CC target sequences, as well as enhanced biological activity. AB071213 to
CC AB072214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC finger peptides which are given in the exemplification of the present
CC invention
CC
XX
XX Sequence 7 AA;
SQ
Query Match 100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRSNLTNR 7
Db 1 DRSNLTNR 7
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Search completed: December 27, 2004, 18:06:44  
Job time : 67.75 secs



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## OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds  
(without alignments)  
29.381 Million cell updates/sec

Title: US-09-846-033B-36  
Perfect score: 7  
Sequence: 1 DRSNLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 4 summaries

Database : Issued Patents AA.\*

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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	US-09-731-558-20	Sequence 20, Appl
2	7	100.0	27	US-09-424-487B-11	Sequence 11, Appl
3	7	100.0	89	US-08-793-408-18	Sequence 18, Appl
4	7	100.0	89	US-09-139-762A-18	Sequence 18, Appl

## ALIGNMENTS

RESULT 1  
US-09-731-558-20  
; Sequence 20, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangam Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; TITLE OF INVENTION: Proteins for the Identification of Gene Function  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; CURRENT FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SBS9  
; OTHER INFORMATION: recognition helix  
US-09-731-558-20

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7  
|||  
Db 1 DRSNLTR 7

RESULT 2  
US-09-424-487B-11  
; Sequence 11, Application US/09424487B  
; Patent No. 6746838  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, YEN  
; APPLICANT: KLUG, AARON  
; APPLICANT: ISALAN, MARK  
; TITLE OF INVENTION: NUCLEIC ACID BINDING PROTEINS  
; FILE REFERENCE: 71278/264975  
; CURRENT APPLICATION NUMBER: US/09/424,487B  
; PRIOR FILING DATE: 2000-02-29  
; CURRENT APPLICATION NUMBER: GB 9710809.6  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: PCT/GB98/01512  
; PRIOR FILING DATE: 1998-05-26  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11  
; LENGTH: 27  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Zinc finger  
; OTHER INFORMATION: peptide  
US-09-424-487B-11

Query Match 100.0%; Score 7; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.064;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRSNLTR 7  
|||  
Db 12 DRSNLTR 18

RESULT 3  
US-08-793-408-18  
; Sequence 18, Application US/08793408  
; Patent No. 6007988  
; GENERAL INFORMATION:  
; APPLICANT: Choo, Yen  
; APPLICANT: Klug, Aaron  
; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Pillsbury Madison & Sutro, L.L.P.  
; STREET: 1100 New York Avenue, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,408  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01949  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9514698.1  
FILING DATE: 18-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9422534.9  
FILING DATE: 08-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9416880.4  
FILING DATE: 20-AUG-1994  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-793-408-18

Query Match  
Best Local Similarity 100.0%; Score 7; DB 3; Length 89;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTTR 7  
|||||  
Db 74 DRSNLTTR 80

RESULT 4  
US-09-139-762A-18  
Sequence 18, Application US/09139762A  
Patent No. 6013453  
GENERAL INFORMATION:  
APPLICANT: Choo, Yen  
APPLICANT: Klug, Aaron  
APPLICANT: Sanchez Garcia, Isidro  
TITLE OF INVENTION: Improvements in or Relating to  
TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/139,762A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/793,408  
FILING DATE: 02-JUN-1997  
APPLICATION NUMBER: PCT/GB95/01949  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9514698.1  
FILING DATE: 18-JUL-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9422534.9  
FILING DATE: 08-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9416880.4  
FILING DATE: 20-AUG-1994  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 89 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-139-762A-18

Query Match  
Best Local Similarity 100.0%; Score 7; DB 3; Length 89;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRSNLTTR 7  
|||||  
Db 74 DRSNLTTR 80

Search completed: December 27, 2004, 18:12:04  
Job time : 16.8 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds  
(without alignments)  
29.381 Million cell updates/sec

Title: US-09-846-033b-35  
Perfect score: 7  
Sequence: 1 RSDNLAR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-731-558-13	Sequence 13, Appl
2	7	100.0	7	4 US-09-779-233-43	Sequence 43, Appl

#### ALIGNMENTS

RESULT 1  
US-09-731-558-13  
; Sequence 13, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Casey, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 7

TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:SB52  
US-09-731-558-13

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDNLAR 7  
Db 1 RSDNLAR 7

RESULT 2  
US-09-779-233-43  
; Sequence 43, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Casey, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; PRIOR FILING DATE: 2001-02-08  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
US-09-779-233-43

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDNLAR 7  
Db 1 RSDNLAR 7

Search completed: December 27, 2004, 18:12:03  
Job time : 15.8 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:30 : Search time 66.75 Seconds  
(without alignments)  
37.620 Million cell updates/sec

Title: US-09-846-033B-34

Perfect score: 7

Sequence: 1 RSDHLAR 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 35872929 residues

Word size : 7

Total number of hits satisfying chosen parameters: 165

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A.GeneSeq.23Sep04:\*

1: - geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	7	100.0	7	4	AAE08727 Human KCA
2	7	100.0	7	5	ABB80792 Human ER-
3	7	100.0	7	5	ABB98019 Zinc fing
4	7	100.0	7	5	ABB98034 Zinc fing
5	7	100.0	7	5	ABP49764 Zinc fing
6	7	100.0	7	5	ABP50067 Zinc fing
7	7	100.0	7	5	ABP48642 Zinc fing
8	7	100.0	7	5	ABP48652 Zinc fing
9	7	100.0	7	5	ABP49518 Zinc fing
10	7	100.0	7	5	ABP49797 Zinc fing
11	7	100.0	7	5	ABP48621 Zinc fing
12	7	100.0	7	5	ABP49260 Zinc fing
13	7	100.0	7	5	ABP50082 Zinc fing
14	7	100.0	7	5	ABP48649 Zinc fing
15	7	100.0	7	5	ABP49794 Zinc fing
16	7	100.0	7	5	ABP49410 Zinc fing
17	7	100.0	7	5	ABP49590 Zinc fing
18	7	100.0	7	5	ABP49515 Zinc fing
19	7	100.0	7	5	ABP49593 Zinc fing
20	7	100.0	7	5	ABP50667 Zinc fing
21	7	100.0	7	5	ABP48662 Zinc fing
22	7	100.0	7	5	ABP49902 Zinc fing
23	7	100.0	7	5	ABP48405 Zinc fing
24	7	100.0	7	5	ABP50064 Zinc fing
25	7	100.0	7	5	ABP50229 Zinc fing

26	7	100.0	7	5	ABP48216	Abp48216 Zinc fing
27	7	100.0	7	5	ABP49242	Abp49242 Zinc fing
28	7	100.0	7	5	ABP49587	Abp49587 Zinc fing
29	7	100.0	7	5	ABP49788	Abp49788 Zinc fing
30	7	100.0	7	5	ABP49791	Abp49791 Zinc fing
31	7	100.0	7	5	ABP50055	Abp50055 Zinc fing
32	7	100.0	7	5	ABP50061	Abp50061 Zinc fing
33	7	100.0	7	5	ABP50292	Abp50292 Zinc fing
34	7	100.0	7	5	ABP50058	Abp50058 Zinc fing
35	7	100.0	7	5	ABP49599	Abp49599 Zinc fing
36	7	100.0	7	5	ABP50079	Abp50079 Zinc fing
37	7	100.0	7	5	ABP49407	Abp49407 Zinc fing
38	7	100.0	7	5	ABP49701	Abp49701 Zinc fing
39	7	100.0	7	5	ABP48993	Abp48993 Zinc fing
40	7	100.0	7	5	ABP50052	Abp50052 Zinc fing
41	7	100.0	7	5	ABP48645	Abp48645 Zinc fing
42	7	100.0	7	5	ABP50085	Abp50085 Zinc fing
43	7	100.0	7	5	ABP49665	Abp49665 Zinc fing
44	7	100.0	7	5	ABP50091	Abp50091 Zinc fing
45	7	100.0	7	5	ABP50226	Abp50226 Zinc fing

## ALIGNMENTS

RESULT 1  
AAE08727 standard; peptide; 7 AA.  
XX  
AC AAE08727;  
XX  
DT 15-NOV-2001 (first entry)  
XX  
DE Human KCA4 protein F1 recognition helix.  
XX  
KW Human; KCA4; EPO; molecular target; zinc finger protein; ZFP;  
KW cellular process; signal transduction; drug-screening.  
XX  
OS Homo sapiens.  
XX  
PN WO200159450-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 08-FEB-2001; 2001WO-US004301.  
XX  
PR 08-FEB-2000; 2000US-0181117P.  
XX  
PS (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
PI Case C;  
XX  
DR WPI; 2001-522491/57.  
XX  
PT Screening compound for interaction with molecular target by contacting  
PT compound with cells; comprising exogenous zinc finger protein that  
PT modulates expression of target, and determining values of properties of  
PT cells.  
XX  
PS Example 10; Page 73; 99pp; English.  
XX  
CC The invention relates to a method of screening a compound for interaction  
CC with a molecular target. The method involves contacting first and second  
CC cells with the compound and determining the values of properties of the  
CC compound. The second cell comprises an exogenous zinc finger protein  
CC (ZFP) that modulates the expression of the molecular target, or isolating  
CC membranes from cell comprising ZFP. The methods allow for high throughput  
CC screening of candidate compound and reduces the incidence of false  
CC positives. The methods are useful for screening a compound for  
CC interaction with a molecular target or for screening a compound for its  
CC effect on a cellular process. The method is useful for testing a compound  
CC for its capacity to transduce a signal to the molecular target or its  
CC capacity to block transduction of a signal through the molecular target.

CC	and for performing biochemical drug-screening assays. The present
CC	sequence is human Kca4 protein recognition helix used in the
CC	exemplification of the invention
XX	
XX	
SO	Sequence 7 AA:
Oy	1 RSDHLAR 7 
Dd	1 RSDHLAR 7
RESULT 2	
ABB80792	100.0%; Score 7; DB 4; Length 7;
ID	ABB80792 standard; peptide; 7 AA.
XX	
AC	ABB80792;
XX	
DT	23-SEP-2002 (first entry)
XX	
DE	Human ER-alpha locus targeting ZFP1 peptide #2.
XX	
KW	ZFP: cytosolic; antidiabetic; ophthalmological; vasotropic; chromatin;
KW	gene expression; antiarthritis; antiarthritic; antipsoriatic; nootropic;
KW	neuroprotective; cerebroprotective; estrogen receptor alpha; ER-alpha;
KV	zinc finger protein.
XX	
OS	Synthetic.
XX	
PN	WO200244386-A2.
PD	06-JUN-2002.
XX	
PF	30-NOV-2001; 2001WO-US045098.
XX	
PR	01-DEC-2000; 2000US-0250804P.
XX	
PA	(SANG-) SANGAMO BIOSCIENCES INC.
XX	
P1	Wolffe AP, Tse C, Collingwood T;
XX	
DR	WPI; 2002-537455/57.
XX	
PT	Regulating expression of gene by contacting cell with regulatory molecule
PT	comprising DNA-binding domain targeted to sequence within accessible
PT	region of cellular chromatin associated with a gene, and functional
PT	domain.
PS	
XX	Example 1; Page 44; 64pp; English.
XX	
CC	The invention relates to regulating the expression of a gene residing in
CC	the chromatin of a cell. The method involves identifying one or more
CC	accessible regions in cellular chromatin associated with gene; designing
CC	a regulatory molecule, where the regulatory molecule comprises a DNA-
CC	binding domain targeted to a sequence within the accessible region, and a
CC	functional domain; and contacting the regulatory molecule with the cell.
CC	The method is used for regulating the expression of a gene (e.g., a gene
CC	encoding a nuclear receptor such as estrogen receptor alpha (Eralpha),
CC	estrogen receptor beta (ERbeta), hepatocyte nuclear factor 4 alpha
CC	(HNF4alpha), hepatocyte nuclear factor 4 gamma (HNF4gamma), peroxisome
CC	proliferator activated receptor gamma (PPARGamma), retinoid X receptor
CC	alpha (RXRalpha), or constitutively active receptor alpha (CARalpha))
CC	residing in the chromatin of a cell. Regulation of gene expression (such
CC	as nuclear receptor genes) will be useful in treatment of various
CC	diseases, including cancer, diabetes and cardiovascular disease, where
CC	the regulatory molecule as described above, is contacted with the cell to
CC	carry out the regulation. The method is also useful for modulation of
CC	gene expression for therapeutic or prophylactic applications e.g.,
CC	diabetic retinopathy, Ischaemia, macular degeneration, rheumatoid
CC	arthritis, psoriasis, HIV infection, sickle cell anemia, Alzheimer's
CC	

[illegible]

CC control of disease states such as tumour metastasis, inflammatory  
 CC diseases, allograft rejection, and for inhibiting processes such as cell  
 CC migration, angiogenesis, and degradation of the basement membrane and/or  
 CC extracellular matrix. Heparanase-targeted DNA binding domains modulates  
 CC gene expression, and are useful for therapeutic or prophylactic  
 CC applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular  
 CC degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell  
 CC anaemia, Alzheimer's disease, muscular dystrophy, neurodegenerative  
 CC diseases, vascular disease, cardiovascular disease, cystic fibrosis,  
 CC stroke, and bacterial, protozoal, fungal and viral infection. Constructs  
 CC of the invention may also be useful in gene therapy. The current sequence  
 CC represents a finger of a three-finger ZFP (zinc finger protein), which  
 CC has a target site in the human heparanase gene

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
 |||||  
 Db 1 RSDHLAR 7

RESULT 4  
 ABB98034  
 ID ABB98034 standard; peptide; 7 AA.  
 XX AC ABB98034;  
 DT 06-SEP-2002 (first entry)  
 XX DE Zinc finger protein 12 finger 1 peptide.  
 XX Human, heparanase; cytototoxic; vasotropic; antidiabetic; anti-HIV;  
 KM ophthalmological; antirheumatic; antiarthritic; antiproliferative;  
 KM antianaemic; neuroprotective; nootropic; cerebroprotective;  
 KM antibacterial; virucide; protozoicide; fungicide; antiinflammatory;  
 KM candidant; immunosuppressive; tumour metastasis; inflammatory disease;  
 KM allograft rejection; cell migration; angiogenesis; basement membrane;  
 KM extracellular matrix; cancer; ischaemia; diabetic retinopathy;  
 KM macular degeneration; rheumatoid arthritis; psoriasis; HIV infection;  
 KM sickle cell anaemia; Alzheimer's disease; muscular dystrophy;  
 KM neurodegenerative disease; vascular disease; cardiovascular disease;  
 KM cystic fibrosis; stroke; gene therapy; zinc finger protein; ZFP.  
 XX Homo sapiens.  
 OS  
 XX WO200244353-A2.  
 PN 06-JUN-2002.  
 PD  
 XX 30-NOV-2001; 2001WO-US044798.  
 PF  
 XX 30-NOV-2000; 2000US-0250690P.  
 PR  
 XX (SANG-) SANGAMO BIOSCIENCES INC.  
 PA  
 XX Wolffe AP, Qi H;  
 XX WPI; 2002-527708/56.  
 DR  
 XX New heparanase polynucleotide, useful for controlling disease states such  
 PT as tumor metastasis, inflammatory diseases and allograft rejection.  
 PT  
 XX Example 3; Page 49; 72pp; English.  
 XX The invention relates to novel heparanase sequences, particularly novel  
 CC sequences from the regulatory regions upstream and downstream of the  
 CC coding region. The activity of polynucleotides of the invention may be  
 CC described as, cytototoxic, vasotropic, antidiabetic, anti-HIV,  
 CC ophthalmological, antirheumatic, antiarthritic, antiproliferative,

CC antianaemic, neuroprotective, nootropic, cerebroprotective,  
 CC antibacterial, virucide, protozoicide, fungicide, antiinflammatory,  
 CC cardiant and immunosuppressive. Modulating expression of heparanase gene  
 CC using constructs of the invention is useful for facilitating targeted  
 CC control of disease states such as tumour metastasis, inflammatory  
 CC diseases, allograft rejection, and for inhibiting processes such as cell  
 CC migration, angiogenesis, and degradation of the basement membrane and/or  
 CC extracellular matrix. Heparanase-targeted DNA binding domains modulates  
 CC gene expression, and are useful for therapeutic or prophylactic  
 CC applications, for e.g. cancer, ischaemia, diabetic retinopathy, macular  
 CC degeneration, rheumatoid arthritis, psoriasis, HIV infection, sickle cell  
 CC anaemia, Alzheimer's disease, muscular dystrophy, neurodegenerative  
 CC diseases, vascular disease, cardiovascular disease, cystic fibrosis,  
 CC stroke, and bacterial, protozoal, fungal and viral infection. Constructs  
 CC of the invention may also be useful in gene therapy. The current sequence  
 CC represents a finger of a three-finger ZFP (zinc finger protein), which  
 CC has a target site in the human heparanase gene

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
 |||||  
 Db 1 RSDHLAR 7

RESULT 5  
 ABP49764  
 ID ABP49764 standard; peptide; 7 AA.  
 XX AC ABP49764;  
 DT 28-AUG-2002 (first entry)  
 XX DE Zinc finger protein related peptide motif SEQ ID NO:2534.  
 XX Zinc finger protein, ZFP; DNA binding protein; zinc finger.  
 KM  
 XX Homo sapiens.  
 OS  
 XX WO200242459-A2.  
 PN 30-MAY-2002.  
 PD  
 XX 20-NOV-2001; 2001WO-US043438.  
 PF  
 XX 20-NOV-2000; 2000US-00716637.  
 PR  
 XX (SANG-) SANGAMO BIOSCIENCES INC.  
 PA  
 XX Liu Q;  
 XX WPI; 2002-500284/53.  
 DR  
 XX New zinc finger protein that binds to target site, useful in studying  
 PT gene function and for human therapeutics and plant engineering, comprises  
 PT first, second and third zinc fingers, ordered from N- to C-terminus.  
 PT  
 XX Example 1; Page 54; 81pp; English.  
 XX The present invention describes a zinc finger protein (I) that binds to a  
 CC target site, comprising a first (F1), a second (F2), and a third (F3)  
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
 CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
 CC (3) designing (M) (1) involves selecting the F1 zinc finger such that it  
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such

CC that it binds to the S3 target subsite, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subsites  
CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determined the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
Db 1 RSDHLAR 7

#### RESULT 6

ABP50067  
ID ABP50067 standard; peptide; 7 AA.

XX ABP50067;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:2635.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

XX 30-MAY-2002.

PF 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

XX WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises

PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 56; 81bp; English.

XX The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
CC that it binds to the S3 target subsite, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subsites  
CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
CC useful in studying gene function, and for human therapeutics and plant

CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determined the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
Db 1 RSDHLAR 7

#### RESULT 7

ABP48642  
ID ABP48642 standard; peptide; 7 AA.

XX ABP48642;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:686.

KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

XX 30-MAY-2002.

PF 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

XX WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 41; 81bp; English.

XX The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
CC that it binds to the S3 target subsite, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subsites  
CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determined the phenotype and function of



CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

XX Sequence 7 AA;

SO Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSDHLAR 7  
1 RSDHLAR 7  
Db

RESULT 8  
ABP48652  
ID ABP48652 standard; peptide; 7 AA.

XX AC ABP48652;

XX DT 28-AUG-2002 (first entry)

XX DE Zinc finger protein related peptide motif SEQ ID NO:894.

XX KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200242459-A2.

XX PD 30-MAY-2002.

XX PF 20-NOV-2001; 2001WO-US043438.

XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PI Liu Q;

XX DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 41; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (II), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present

CC invention  
XX Sequence 7 AA;

SO Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSDHLAR 7  
1 RSDHLAR 7  
Db

RESULT 9  
ABP49518  
ID ABP49518 standard; peptide; 7 AA.

XX AC ABP49518;

XX DT 28-AUG-2002 (first entry)

XX DE Zinc finger protein related peptide motif SEQ ID NO:1748.

XX KM Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200242459-A2.

XX PD 30-MAY-2002.

XX PF 20-NOV-2001; 2001WO-US043438.

XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PI Liu Q;

XX DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 51; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (II), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

SO Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
Db 1 RSDHLAR 7

## RESULT 10

ABP49797  
ID ABP49797 standard; peptide; 7 AA.

AC ABP49797;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:2545.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

PD 30-MAY-2002.

PF 20-NOV-2001; 2001MO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 54; 81bp; English.

CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
CC that it binds to the S3 target subsite, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subsites  
CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
Db 1 RSDHLAR 7

## RESULT 11

ABP48621  
ID ABP48621 standard; peptide; 7 AA.

AC ABP48621;

DT 28-AUG-2002 (first entry)

DE Zinc finger protein related peptide motif SEQ ID NO:679.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger.

XX Homo sapiens.

OS Synthetic.

PN WO200242459-A2.

PD 30-MAY-2002.

PF 20-NOV-2001; 2001MO-US043438.

PR 20-NOV-2000; 2000US-00716637.

PA (SANG-) SANGAMO BIOSCIENCES INC.

PI Liu Q;

DR WPI; 2002-500284/53.

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 41; 81bp; English.

CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
CC that it binds to the S3 target subsite, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subsites  
CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determine the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
Db 1 RSDHLAR 7

RESULT 12  
ABP49260  
ID ABP49260 standard; peptide; 7 AA.  
XX  
XX  
AC ABP49260;  
XX  
XX  
DT 28-AUG-2002 (first entry)  
XX  
XX  
DE Zinc finger protein related peptide motif SEQ ID NO:1388.  
XX  
XX  
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN MO200242459-A2.  
XX  
XX  
PD 30-MAY-2002.  
XX  
XX  
PF 20-NOV-2001; 2001WO-US043438.  
XX  
XX  
PR 20-NOV-2000; 2000US-00716637.  
XX  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
XX  
PI Liu Q;  
XX  
XX  
DR WPI; 2002-500284/53.  
XX  
XX  
PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX  
XX  
PS Example 1; Page 48; 81pp; English.  
XX  
XX  
CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determined the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention  
XX  
XX  
SQ Sequence 7 AA;  
XX

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
| | | | |  
| | | | |  
Db 1 RSDHLAR 7

RESULT 13  
ABP50082  
ID ABP50082 standard; peptide; 7 AA.

XX  
XX  
AC ABP50082;  
XX  
XX  
DT 28-AUG-2002 (first entry)  
XX  
XX  
DE Zinc finger protein related peptide motif SEQ ID NO:2640.  
XX  
XX  
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
PN MO200242459-A2.  
XX  
XX  
PD 30-MAY-2002.  
XX  
XX  
PF 20-NOV-2001; 2001WO-US043438.  
XX  
XX  
PR 20-NOV-2000; 2000US-00716637.  
XX  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
XX  
PI Liu Q;  
XX  
XX  
DR WPI; 2002-500284/53.  
XX  
XX  
PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX  
XX  
PS Example 1; Page 56; 81pp; English.  
XX  
XX  
CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target sub-site. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target sub-site, selecting the F2 zinc finger such that it  
CC binds to the S2 target sub-site, and selecting the F3 zinc finger such  
CC that it binds to the S3 target sub-site, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target sub-sites  
CC having the nucleotide G in the 5'-most position of the sub-site. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determined the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention  
XX  
XX  
SQ Sequence 7 AA;  
XX

Query Match 100.0%; Score 7; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
| | | | |  
| | | | |  
Db 1 RSDHLAR 7

RESULT 14  
ABP48649  
ID ABP48649 standard; peptide; 7 AA.  
XX  
XX  
AC ABP48649;  
XX  
XX  
DT 28-AUG-2002 (first entry)

```

XX  Zinc finger protein related peptide motif SEQ ID NO:893.
DE  Zinc finger protein; ZFP, DNA binding protein, zinc finger.
XX
XX  Homo sapiens.
OS  Synthetic.
XX
XX  WO200242459-A2.
XX
XX  30-MAY-2002.
XX
XX  20-NOV-2001; 2001WO-US043438.
XX
XX  20-NOV-2000; 2000US-00716637.
XX
XX  (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX  Liu Q;
XX
XX  WPI; 2002-500284/53.
XX
XX  New zinc finger protein that binds to target site, useful in studying
PT  gene function and for human therapeutics and plant engineering, comprises
PT  first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX  Example 1; Page 41; 81pp; English.
XX
XX  The present invention describes a zinc finger protein (I) that binds to a
CC  target site, comprising a first (F1), a second (F2), and a third (F3)
CC  zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC  target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC  and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC  (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC  (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC  binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC  binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC  that it binds to the S3 target sub-site, thus designing (I) that binds to
CC  a target site. (I) is useful for recognition of triplet target sub-sites
CC  having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC  useful in studying gene function, and for human therapeutics and plant
CC  engineering. (I), (II) or (III) is useful in therapeutic methods to
CC  modulate the expression of a target region within a subject, in
CC  diagnostic methods for sequence specific detection of target nucleic acid
CC  in a sample, and in assays to determined the phenotype and function of
CC  gene expression. (I) has improved affinity and specificity for their
CC  target sequences, as well as enhanced biological activity. ABQ71213 to
CC  ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC  finger peptides which are given in the exemplification of the present
CC  invention
XX
XX  Sequence 7 AA;
SQ

```

```

Query Match      100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY  1 RSDHLAR 7
    |||||
Db  1 RSDHLAR 7

```

```

RESULT 15
ABP49794
ID  ABP49794 standard; peptide; 7 AA.
XX
XX  ABP49794;
AC
XX
XX  28-AUG-2002 (first entry)
DT
XX
XX  Zinc finger procein related peptide motif SEQ ID NO:2544.
DE
XX
XX  Zinc finger protein; ZFP; DNA binding protein; zinc finger.
KM

```

```

XX  Homo sapiens.
OS  Synthetic.
XX
XX  WO200242459-A2.
XX
XX  30-MAY-2002.
XX
XX  20-NOV-2001; 2001WO-US043438.
XX
XX  20-NOV-2000; 2000US-00716637.
XX
XX  (SANG-) SANGAMO BIOSCIENCES INC.
XX
XX  Liu Q;
XX
XX  WPI; 2002-500284/53.
XX
XX  New zinc finger protein that binds to target site, useful in studying
PT  gene function and for human therapeutics and plant engineering, comprises
PT  first, second and third zinc fingers, ordered from N- to C-terminus.
XX
XX  Example 1; Page 54; 81pp; English.
XX
XX  The present invention describes a zinc finger protein (I) that binds to a
CC  target site, comprising a first (F1), a second (F2), and a third (F3)
CC  zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
CC  target site comprises, in 3'-5' direction, a first (S1), a second (S2),
CC  and a third (S3) target sub-site. Also described are: (1) a polypeptide
CC  (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
CC  (3) designing (M) (I) involves selecting the F1 zinc finger such that it
CC  binds to the S1 target sub-site, selecting the F2 zinc finger such that it
CC  binds to the S2 target sub-site, and selecting the F3 zinc finger such
CC  that it binds to the S3 target sub-site, thus designing (I) that binds to
CC  a target site. (I) is useful for recognition of triplet target sub-sites
CC  having the nucleotide G in the 5'-most position of the sub-site. (I) is
CC  useful in studying gene function, and for human therapeutics and plant
CC  engineering. (I), (II) or (III) is useful in therapeutic methods to
CC  modulate the expression of a target region within a subject, in
CC  diagnostic methods for sequence specific detection of target nucleic acid
CC  in a sample, and in assays to determined the phenotype and function of
CC  gene expression. (I) has improved affinity and specificity for their
CC  target sequences, as well as enhanced biological activity. ABQ71213 to
CC  ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
CC  finger peptides which are given in the exemplification of the present
CC  invention
XX
XX  Sequence 7 AA;
SQ

```

```

Query Match      100.0%; Score 7; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY  1 RSDHLAR 7
    |||||
Db  1 RSDHLAR 7

```

```

Search completed: December 27, 2004, 18:06:43
Job time : 67.75 secs

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 27, 2004, 17:02:31 ; Search time 15.8 Seconds

(without alignments)  
29.381 Million cell updates/sec

Title: US-09-846-033B-34

Perfect score: 7

Sequence: 1 RSDHLAR 7

Scoring table: OLIGO

Searched: Gapop 60.0 , Gapext 60.0

Word size : 7

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	4 US-09-779-233-42	Sequence 42, Appl
2	7	100.0	100	4 US-09-248-796A-16192	Sequence 16192, A

## ALIGNMENTS

RESULT 1  
US-09-779-233-42  
; Sequence 42, Application US/09779233  
; Patent No. 6689558  
; GENERAL INFORMATION:  
; APPLICANT: Case, Casey  
; TITLE OF INVENTION: CELLS FOR DRUG DISCOVERY  
; FILE REFERENCE: 8325-0010  
; CURRENT APPLICATION NUMBER: US/09/779,233  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: recognition  
US-09-779-233-42

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
|||||  
DB 1 RSDHLAR 7

RESULT 2  
US-09-248-796A-16192  
; Sequence 16192, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstein et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 16192  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-16192

Query Match 100.0%; Score 7; DB 4; Length 100;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLAR 7  
|||||  
DB 57 RSDHLAR 63

Search completed: December 27, 2004, 18:12:03  
Job time : 15.8 secs

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## OM protein - protein search, using sw model

Run on: December 27, 2004, 20:31:09 ; Search time 16.35 Seconds  
(without alignments)  
28.393 Million cell updates/sec

Title: US-09-846-033B-99

Perfect score: 7  
Sequence: 1 RSDALRQ 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query				
No.	Score	Match	Length	ID	Description
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No matches found					

Search completed: December 27, 2004, 21:40:38  
Job time : 17.35 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-98

Perfect score: 7  
Sequence: 1 RSDALAR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	881	3	US-09-413-814-44 Sequence 44, Appl

#### ALIGNMENTS

RESULT 1  
US-09-413-814-44  
; Sequence 44, Application US/09413814  
; Patent No. 6225064  
; GENERAL INFORMATION:  
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH  
; APPLICANT: Bristol-Myers Squibb, Co.  
; APPLICANT: Beyer, Stefan  
; APPLICANT: Bioecker, Helmut  
; APPLICANT: Brandt, Petra  
; APPLICANT: Cino, Paul M  
; APPLICANT: Dougherty, Brian A  
; APPLICANT: Goldberg, Steven L  
; APPLICANT: Hofle, Gerhard  
; APPLICANT: Mueller, Joachim  
; APPLICANT: Reichenbach, Hans  
; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or  
; TITLE OF INVENTION: heteropolypeptide compounds  
; FILE REFERENCE: PCT/US 99/23535  
; CURRENT APPLICATION NUMBER: US/09/413,814  
; CURRENT FILING DATE: 1999-10-07

; EARLIER APPLICATION NUMBER: DE 198 46 493.2  
; EARLIER FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 881  
; TYPE: PRT  
; ORGANISM: Sorangium cellulosum  
US-09-413-814-44

Query Match 100.0%; Score 7; DB 3; Length 881;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RSDALAR 7  
Db 295 RSDALAR 301

Search completed: December 27, 2004, 20:31:05  
Job time : 16.85 secs

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# OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033b-97  
Perfect score: 7  
Sequence: 1 QSGSLTR 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	4	US-09-731-558-16 Sequence 16, Appl

## ALIGNMENTS

RESULT 1  
US-09-731-558-16  
; Sequence 16, Application US/09731558  
; Patent No. 6503717  
; GENERAL INFORMATION:  
; APPLICANT: Casey, Casey Christopher  
; APPLICANT: Liu, Qiang  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Methods of Using Randomized Libraries of Zinc Finger  
; FILE REFERENCE: 019496-003210US  
; CURRENT APPLICATION NUMBER: US/09/731,558  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: US 09/456,100  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 7  
; TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SBSS  
; OTHER INFORMATION: recognition helix  
US-09-731-558-16

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0;

QY 1 QSGSLTR 7  
|||  
Db 1 QSGSLTR 7

Search completed: December 27, 2004, 20:31:04  
Job time : 15.85 secs

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## OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-96

Perfect score: 7  
Sequence: 1 RSDALSA 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 7

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
-----					
No matches found					

Search completed: December 27, 2004, 20:31:04  
Job time : 15.85 secs

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## OM protein - protein search, using sw model

Run on: December 27, 2004, 19:21:38 ; Search time 15.85 Seconds  
(without alignments)  
29.289 Million cell updates/sec

Title: US-09-846-033B-95

Perfect score: 7

Sequence: 1 RSDHLTT 7

Scoring table: OLIGO

Searched: 478139 seqs, 6631800 residues

Word size : 7

Total number of hits satisfying chosen parameters: 59

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6C.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/6D.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	US-09-614-679A-19	Sequence 19, Appl
2	7	100.0	10	US-09-139-762A-19	Sequence 19, Appl
3	7	100.0	10	US-09-139-762A-53	Sequence 53, Appl
4	7	100.0	20	US-08-040-548-19	Sequence 19, Appl
5	7	100.0	20	US-08-466-344-19	Sequence 19, Appl
6	7	100.0	21	US-09-229-007A-95	Sequence 95, Appl
7	7	100.0	21	US-10-113-424-95	Sequence 95, Appl
8	7	100.0	26	US-08-620-151-111	Sequence 111, Appl
9	7	100.0	28	US-08-040-548-34	Sequence 34, Appl
10	7	100.0	28	US-08-466-344-34	Sequence 34, Appl
11	7	100.0	28	US-09-058-459-1	Sequence 1, Appl
12	7	100.0	28	US-09-127-926-1	Sequence 1, Appl
13	7	100.0	28	US-09-037-179B-15	Sequence 15, Appl
14	7	100.0	28	US-09-240-179-2	Sequence 2, Appl
15	7	100.0	28	US-09-714-357-1	Sequence 7, Appl
16	7	100.0	28	US-09-500-700-70	Sequence 70, Appl
17	7	100.0	28	US-09-716-637-13	Sequence 13, Appl
18	7	100.0	59	US-08-040-548-7	Sequence 7, Appl
19	7	100.0	59	US-08-466-344-7	Sequence 7, Appl
20	7	100.0	85	US-09-229-007A-8	Sequence 8, Appl
21	7	100.0	85	US-10-113-424-8	Sequence 8, Appl
22	7	100.0	85	US-06152-3	Patent No. 5206152
23	7	100.0	87	US-10-057-552-1	Sequence 1, Appl
24	7	100.0	89	US-08-040-548-8	Sequence 8, Appl
25	7	100.0	89	US-08-466-344-8	Sequence 8, Appl
26	7	100.0	91	US-08-863-813A-5	Sequence 5, Appl
27	7	100.0	91	US-08-676-318A-5	Sequence 5, Appl

28	7	100.0	91	US-09-500-700-5	Sequence 5, Appl
29	7	100.0	109	US-08-224-482-11	Sequence 11, Appl
30	7	100.0	153	US-08-863-813A-34	Sequence 34, Appl
31	7	100.0	153	US-08-863-813A-36	Sequence 36, Appl
32	7	100.0	153	US-08-676-318A-34	Sequence 34, Appl
33	7	100.0	153	US-08-676-318A-36	Sequence 36, Appl
34	7	100.0	153	US-09-500-700-34	Sequence 34, Appl
35	7	100.0	153	US-09-500-700-36	Sequence 36, Appl
36	7	100.0	181	US-08-863-813A-44	Sequence 44, Appl
37	7	100.0	181	US-08-676-318A-44	Sequence 44, Appl
38	7	100.0	181	US-09-500-700-44	Sequence 44, Appl
39	7	100.0	387	US-08-224-482-8	Sequence 8, Appl
40	7	100.0	387	US-09-538-092-1278	Sequence 1278, Ap
41	7	100.0	453	US-06152-7	Patent No. 5206152
42	7	100.0	453	US-08-224-482-6	Sequence 6, Appl
43	7	100.0	456	US-08-040-548-2	Sequence 2, Appl
44	7	100.0	456	US-08-466-344-2	Sequence 2, Appl
45	7	100.0	456	US-09-919-039-66	Sequence 66, Appl

## ALIGNMENTS

RESULT 1  
US-09-614-679A-19  
Sequence 19, Application US/09614679A  
Patent No. 6492117  
GENERAL INFORMATION:  
APPLICANT: CHOO, YEN  
APPLICANT: ISALAN, MARK  
APPLICANT: BALSBRAMANTAN, SHANKAR  
APPLICANT: LIU, XIAOHAI  
TITLE OF INVENTION: MOLECULES  
FILE REFERENCE: 71278/271599  
CURRENT APPLICATION NUMBER: US/09/614, 679A  
CURRENT FILING DATE: 2000-07-12  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 19  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-614-679A-19  
Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 RSDHLTT 7  
Db 1 RSDHLTT 7  
RESULT 2  
US-09-139-762A-19  
Sequence 19, Application US/09139762A  
Patent No. 6013453  
GENERAL INFORMATION:  
APPLICANT: Choo, Yen  
APPLICANT: Kluug, Aaron  
APPLICANT: Sanchez Garcia, Isidro  
TITLE OF INVENTION: Improvements in or Relating to  
TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.

COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/139,762A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/793,408  
FILING DATE: 02-JUN-1997  
APPLICATION NUMBER: PCT/GB95/01949  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9514698.1  
FILING DATE: 18-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9422534.9  
FILING DATE: 08-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9416880.4  
FILING DATE: 20-AUG-1994  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-139-762A-19

Query Match 100.0%; Score 7; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
DB 1 RSDHLTT 7

RESULT 3  
US-09-139-762A-53  
Sequence 53, Application US/09139762A  
Patent No. 6013453  
GENERAL INFORMATION:  
APPLICANT: Choo, Yen  
APPLICANT: Klug, Aaron  
APPLICANT: Sanchez Garcia, Isidro  
TITLE OF INVENTION: Improvements in or Relating to  
TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/139,762A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/793,408  
FILING DATE: 02-JUN-1997

APPLICATION NUMBER: PCT/GB95/01949  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9514698.1  
FILING DATE: 18-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9422534.9  
FILING DATE: 08-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9416880.4  
FILING DATE: 20-AUG-1994  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-139-762A-53

Query Match 100.0%; Score 7; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.017;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
DB 1 RSDHLTT 7

RESULT 4  
US-08-040-548-19  
Sequence 19, Application US/08040548  
Patent No. 5763209  
GENERAL INFORMATION:  
APPLICANT: Sukhtme, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5763209th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/040,548  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arc0067  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-040-548-19

Query Match 100.0%; Score 7; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 RSDHLLT 7  
Db 9 RSDHLLT 15

## RESULT 5

US-08-466-344-19  
; Sequence 19, Application US/08466344  
; Patent No. 5773583  
; GENERAL INFORMATION:  
; APPLICANT: Sukhame, Vikas P.  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5773583th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: U.S.A.  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,344  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/040,548  
; FILING DATE: 31-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coughlin, Daniel F.  
; REGISTRATION NUMBER: 36,111  
; REFERENCE/DOCKET NUMBER: arc0607  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 744-0090  
; TELEFAX: (312) 245-4961  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-466-344-19

Query Match 100.0%; Score 7; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLLT 7  
Db 9 RSDHLLT 15

## RESULT 6

US-09-229-007A-95  
; Sequence 95, Application US/09229007A  
; Patent No. 6453242  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins  
; TITLE OF INVENTION: to Bind to Preselected Sites

FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/09/229,007A  
; CURRENT FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 21  
; TYPE: PRT

ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence  
US-09-229-007A-95

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.033;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLLT 7  
Db 8 RSDHLLT 14

## RESULT 7

US-10-113-424-95  
; Sequence 95, Application US/10113424  
; Patent No. 6785613  
; GENERAL INFORMATION:  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Case, Casey C.  
; APPLICANT: Cox III, George N.  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Rebar, Edward J.  
; APPLICANT: Sangamo Biosciences, Inc.  
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger  
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins  
; TITLE OF INVENTION: to Bind to Preselected Sites  
; FILE REFERENCE: 019496-001800US  
; CURRENT APPLICATION NUMBER: US/10/113,424  
; CURRENT FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US/09/229,007A  
; PRIOR FILING DATE: 1999-01-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 95  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: ZFP sequence  
; OTHER INFORMATION: (F1, F2 and F3) from Zif 268  
US-10-113-424-95

Query Match 100.0%; Score 7; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.033;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSDHLLT 7  
Db 8 RSDHLLT 14

## RESULT 8

US-08-620-151-111  
; Sequence 111, Application US/08620151  
; Patent No. 5928955  
; GENERAL INFORMATION:  
; APPLICANT: Imperiali, Barbara  
; APPLICANT: Walkup, Grant K.  
; TITLE OF INVENTION: PEPTIDYL FLUORESCENT CHEMOSENSOR FOR  
; TITLE OF INVENTION: DIVALENT ZINC  
; NUMBER OF SEQUENCES: 136  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: BRINKS, HOFER, GILSON & LIONE  
STREET: NBC Tower - Suite 3600, 455 N. Cityfront  
STREET: Plaza Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60611-5599  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,151  
FILING DATE: 22-MAR-1996  
CLASSIFICATION: 422  
ATTORNEY/AGENT INFORMATION:  
NAME: Shannon, Karen L.  
REGISTRATION NUMBER: 36,675  
REFERENCE/DOCKET NUMBER: 8597/6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-321-4200  
TELEFAX: 312-321-4239  
INFORMATION FOR SEQ ID NO: 111:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-620-151-111

Query Match 100.0%; Score 7; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 13 RSDHLTT 19

RESULT 9  
US-08-040-548-34  
Sequence 34, Application US/08040548  
Patent No. 5763209  
GENERAL INFORMATION:  
APPLICANT: Sukhame, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5763209th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/040,548  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961

INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-040-548-34

Query Match 100.0%; Score 7; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 9 RSDHLTT 15

RESULT 10  
US-08-466-344-34  
Sequence 34, Application US/08466344  
Patent No. 5773583  
GENERAL INFORMATION:  
APPLICANT: Sukhame, Vikas P.  
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: 321 No. 5773583th Clark Street, Suite 800  
CITY: Chicago  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60610  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,344  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/040,548  
FILING DATE: 31-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Coughlin, Daniel F.  
REGISTRATION NUMBER: 36,111  
REFERENCE/DOCKET NUMBER: arcd067  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 744-0090  
TELEFAX: (312) 245-4961  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-466-344-34

Query Match 100.0%; Score 7; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLTT 7  
Db 9 RSDHLTT 15

RESULT 11  
US-09-058-459-1

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; Sequence 1, Application US/09058459
; Patent No. 618965
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahljat, Basil I.
; APPLICANT: Gordon, D. B.
; APPLICANT: Street, Arthur
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN
; FILE REFERENCE: A65353-3/RFT/RMS/SCR
; CURRENT APPLICATION NUMBER: US/09/058,459
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/043,464
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/054,678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061,097
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mouse
US-09-058-459-1

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSDHLTT 7
Db      14 RSDHLTT 20

RESULT 12
US-09-127-926-1
; Sequence 1, Application US/09127926
; Patent No. 6269312
; GENERAL INFORMATION:
; APPLICANT: Mayo, Stephen L.
; APPLICANT: Dahljat, Basil I.
; APPLICANT: Gordon, D. Benjamin
; APPLICANT: Street, Arthur
; APPLICANT: Su, Yaoying
; TITLE OF INVENTION: Apparatus and Method for Automated Protein Design
; FILE REFERENCE: A65353-4/RFT/RMS/SCR
; CURRENT APPLICATION NUMBER: US/09/127,926
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/043,464
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/054,678
; PRIOR FILING DATE: 1997-08-04
; PRIOR APPLICATION NUMBER: 60/061,097
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: 09/058,459
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/087,561
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Mouse
US-09-127-926-1

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSDHLTT 7
Db      14 RSDHLTT 20

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RESULT 13
US-09-037-179B-15
; Sequence 15, Application US/09037179B
; Patent No. 6316599
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; FILE REFERENCE: 0050.1312-011
; CURRENT APPLICATION NUMBER: US/09/037,179B
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: US 08/102,942
; PRIOR FILING DATE: 1993-08-02
; PRIOR APPLICATION NUMBER: US 07/614,161
; PRIOR FILING DATE: 1990-11-13
; PRIOR APPLICATION NUMBER: US 07/435,780
; PRIOR FILING DATE: 1989-11-13
; PRIOR APPLICATION NUMBER: US 07/795,323
; PRIOR FILING DATE: 1994-09-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-037-179B-15

Query Match
Best Local Similarity 100.0%; Score 7; DB 3; Length 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RSDHLTT 7
Db      17 RSDHLTT 23

RESULT 14
US-09-240-179-2
; Sequence 2, Application US/09240179
; Patent No. 6410248
; GENERAL INFORMATION:
; APPLICANT: Greisman, Harvey A.
; APPLICANT: Pabo, Carl O.
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: A General Strategy for Selecting High-Affinity Zinc
; FILE REFERENCE: 019496-000220US
; CURRENT APPLICATION NUMBER: US/09/240,179
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: US 60/073,223
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Zlf268 zinc
; OTHER INFORMATION: finger 2
US-09-240-179-2

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Query Match 100.0%; Score 7; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLYT 7  
Db 13 RSDHLYT 19

RESULT 15  
US-09-714-357-1

; Sequence 1, Application US/09714357  
; Patent No. 6708120  
; GENERAL INFORMATION:  
; APPLICANT: Mayo, Stephen L.  
; APPLICANT: Dahiya, Baasill I.  
; APPLICANT: Gordon, D. B.  
; APPLICANT: Street, Arthur  
; TITLE OF INVENTION: APPARATUS AND METHOD FOR AUTOMATED PROTEIN DESIGN  
; FILE REFERENCE: A65353-3/RPT/RMS/SJR  
; CURRENT APPLICATION NUMBER: US/09/714,357  
; CURRENT FILING DATE: 2000-11-15  
; PRIOR APPLICATION NUMBER: 09/058,459  
; PRIOR FILING DATE: 1998-04-10  
; PRIOR APPLICATION NUMBER: 60/054,678  
; PRIOR FILING DATE: 1997-08-04  
; PRIOR APPLICATION NUMBER: 60/061,097  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 28  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-714-357-1

Query Match 100.0%; Score 7; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSDHLYT 7  
Db 14 RSDHLYT 20

Search completed: December 27, 2004, 20:31:04  
Job time : 15.85 secs